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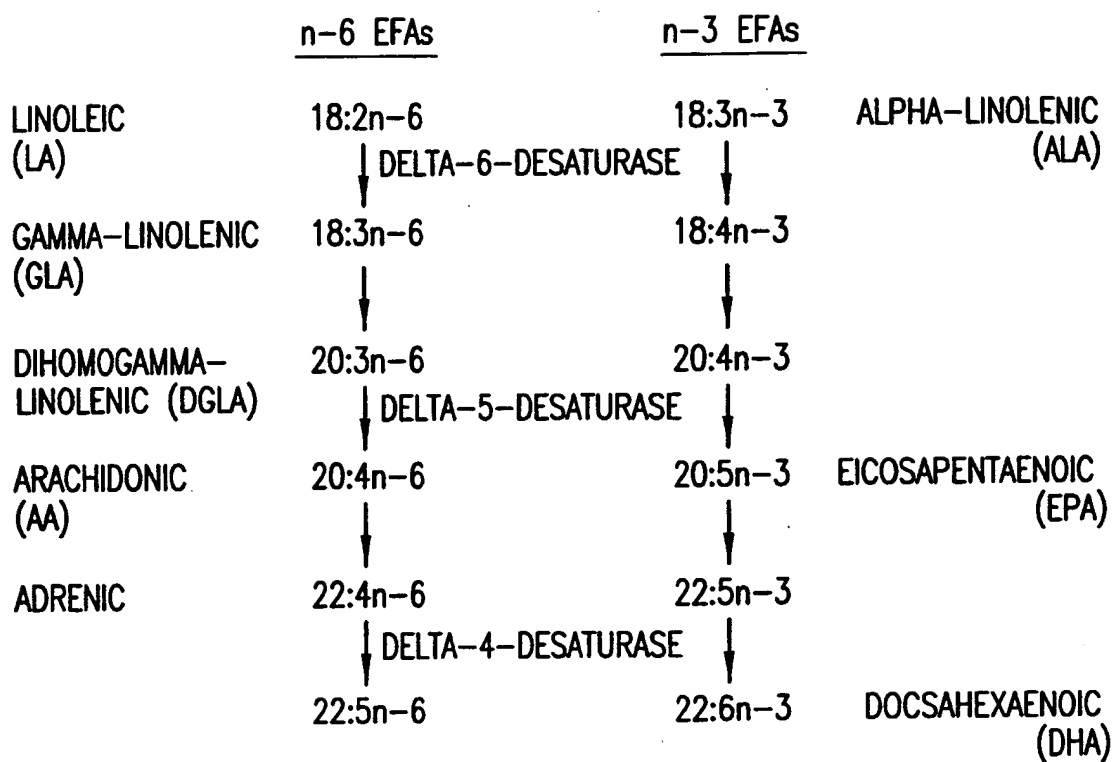


FIG.1

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0906088-074304

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151 gtgccccggg gcagggtgg gtggcgccg ctgtcctccc gggaggggag
201 ggcgcctcg acgcgcctt ccctggcgcc caatggagac cgaggccccg
251 cgcctggatt ggagcggacg cgggggtcag ccagccttgg gggccggggc
301 ctggccgggg gcgggggggc aggcgaggcg aggcgggcgc cgtccgcgcg
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501 ACCTCGGCCA CCGCCTGGGA TCCCAGGAC TCGTGCCTGC AGCATGGGCG
551 GCGTCGGGGA GCCGGGACCG CGGGAGGGAC CCGGCAGACC GGGGGCGCCG
601 CTGCCCACCT TCTGCTGGGA GCAGATCCGC GCGCACGACC AGCCCGGCCA
651 CAAGTGCTTG GTCATCGAGC GCCGCGCTTA CGACATCAGC CGCTGGGCAC
701 AGCGGCACCC AGGGGGCAGC CGCCTCATCG GCCACCACGG CGCTGAGGAC
751 GCCACGgtaa ggaagccata aggaagccac ccaccggcgg gtggagcctg
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2301 cccagactgg agtgcaatgg cgccatcttg gctcactgca acctccgcct
2351 cccaggttca agcgattctc ctgcctcagc ctcccagta gctgggatta
2401 cgggcacgcg ccaccacgce cagcatattg tatttttagt agagacgggg
2451 tttcaccatg ttggccaagc tgggtctcgaa ctccctgacct cgtgatccac
2501 ccacctcggc ctcccaaagt gctgggatta caggcgtgag ccaccacgcc
2551 cggctgggat acagaaagct tttatttcat cactgtttcc tgccctgggtgc

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FIG.2A

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2601 caggcccatg ctgggggttcc tcccaagtgg aattactgac ttaacattta  
 2651 gcttgggatc ctgagacttc catcacacag ttttctcatt gattcgcagc  
 2701 caataatatc tgttttaaaa acatctcagg ccgagcgctg tggctcacac  
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 2801 gggagtttga gaccagcctg accaacaatgg agaaaccctg tctcttctaa  
 2851 aaaaatacaa aattagccag gcgtggtggc gcatgcctgt aatcccagca  
 2901 ctttgggagg ctgaggcagg agaatcgctt gaaccagga gacggagggt  
 2951 ccggtgagcc gagatcgcg ctttgactc cagcctgggc aacaagagca  
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 3101 tgtcactcct ctgtgcccc a gtttactcat ctgtaaagtg ggagagctgg  
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 3251 taagtgtgag cgtgccctgc aaactgcagc gtatggtggg acagccctgc  
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 4001 cacttgacag atgagaaaac agaggctcag agaggcaaag tggctgaaa  
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 5201 gccattttg tagatgagga gactgagttt gaaactgggg ggtgtaatgg  
 5251 aaccttctca ggacccttga agggtagggc ctttgtactc gggccacgag

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FIG.2B

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 5351 ggcagatctg aggccacagg agttgggttg ggggtggctc cagagccact  
 5401 ccactccctc ctaccacatt gactgccttg aaagtccctt aatggccact  
 5451 cccatgaagt gtgactgctc tgggctcccc gcaggcgttt tctgcaaggc  
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 7701 ctggactctg atctaacctc ggtcaaatgg aactgtgtga ccttgaagaa  
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 7801 aggagaggcc cacagaggac caggtcacat gacctcagcc agttccagag  
 7851 aaggctgttt gcttccaggt ttccggcctga gtccaggccc ctgccctact  
 7901 cgcactccct gatagcatga gaagcacagc cccagggtgc ccaccagct  
 7951 ctgagagccc agcctgcttc ccagggaact gtcacagccc cacctgtccc

FIG.2C

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8001 ttccccagct ggagccctgt caatggcttt ggggttctct gacacagccc  
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 10301 aataggaggc ccctgtcctc agtcagcttt cttcaaagggt gtttccctta  
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 10551 gagcccagggt gtgaagtcca agcttacttt acttctgggc cacttctggtg  
 10601 ctggtctctt tccctggccc ttatctttct cctggtctgt cttctcttct  
 10651 caccctctt ctttactct tcttcttct cctgcatcgt actccacccc

FIG.2D

[illegible]

FIG. 2E

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13301 CCACTGGTGG AACTTCCGCC ACTTCCAGCA CCACGCCAAG CCCAACATCT  
 13351 TCCACAAAGA CCCAGACGTG ACGGTGGCGC CCGTCTTCCT CCTGGGGGAG  
 13401 TCATCCGTCG AGgtgggtgg ggaggggacct ggacaacctc tggctggggc  
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 13751 CACCTGTACT TCTTCTGAg tgagtgtcca tctgtccttc tggggtgggg  
 13801 gagtgcctgg gcctgcactg tcctccctgc tgtcctggac cactcccagc  
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 14601 ctgtacgtgt ggtggggggg ggttgaggaa cagggggggt gtgggtctct  
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 14901 ggctccaga cctccgggca cctggagacc tctcggtatc gcctctgccc  
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 15001 TATCTACCT CCCCTCTAC GCGTCCCTG GGGTGTCTGT CTCTTTGTT  
 15051 GCTGTCAggt atggcaggga gtggcgaggt cacacacagg cgacagggtga  
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 15251 gtaagtggcc cggtgggtgt cggagctgct ctggactcag cctcacagt  
 15301 gacactgtc cattcagatt ctttaaacac tggcaagggt gcgatggcca  
 15351 caatcctatt gtacagataa ggaagtcaag gccacttggg gacagctgct  
 15401 ctccagcctc cactcagggt gcctaagtgg tgagctggac ctagggcagt  
 15451 gcccagacct cccacagGG TCCTGGAAAG CCACTGGTTC GTGTGGATCA  
 15501 CACAGATGAA CCACATCCCC AAGGAGATCG GCCACGAGAA GCACCGGGAC  
 15551 TGGGTCAGCT CTCAGgtggg cagcagggtt ggggcccac ctgggtgggg  
 15601 tggggggtcc cagctaggag ccagatggca aagcagggt gagggcctga  
 15651 cggggctgcc aggtggggga tgggtccgtg gggtcaggga tctgcaacgg  
 15701 cctctcaca tgtgccccgc cggttccgg cagCTGGCAG CCACCTGCAA  
 15751 CGTGGAGCCC TCACTTTTCA CCAACTGGTT CAGCGGGCAC CTCAACTTCC  
 15801 AGATCGAGCA CCAgtgagtg tgggtgctgg gggccagtgg gaggtgggga  
 15851 gggggtcctg ggaggggatc ctgggagggg acccggtgggt ggggcctctc

FIG.2F

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15901 tctggaatct cccacttcag gtgccagcat acgctcccca cccccagCCT  
 15951 CTTCCCCAGG ATGCCGAGAC ACAACTACAG CCGGGTGGCC CCGCTGGTCA  
 16001 AGTCGCTGTG TGCCAAGCAC GGCCTCAGCT ACGAAGTGAA GCCCTTCCTC  
 16051 ACCGCGCTGG TGGACATCGT CAGgtgaggc tgcagcccg cccctctgtt  
 16101 ctggtggctt ccccagggcc tatgcctacc cttgtccagg tcagcctcat  
 16151 gctgagcccc cagggctccct gaggctttct gtccacgtcc catgcccttc  
 16201 ctcccttccc cagccttcac gcacacagtg agaattttctg gagcacctac  
 16251 tgcagactca caaacagcag tgcctgcggt gagcaggctc atgcaaacct  
 16301 acccccaaag gctgaggga gaaagctaac agatccagtt tctcagaagg  
 16351 aaacacttaa cagggactca taaacagaag ccatgtctca gggccgggtg  
 16401 cgggtggctca cgcctgtaat tccagcactt ggggaggctg aggtgggctg  
 16451 atcacttgag gtcaggagt cgagaccagc ctggccaaca tggtgaaacc  
 16501 ccgtctctac taaaaaaaaa aaaaaaaaaa aaaacaaaac aaaaattagc  
 16551 tgggtgtggt ggcagggtgcc cataatccca gctacttggg aggtgaggg  
 16601 aggagaatca cttgaactcg caggggcaga ggttgcagtg agctgagatt  
 16651 gtgcctttgc agtccagcct gggcaacaga gcaagactct ctcaaaaaca  
 16701 aacaaaaaaa ccatgtctca ggcagccaag agttgggaca tcccctcaca  
 16751 cgccctctag aaagaaccct ctatatagca agcttttagg gtgaacccca  
 16801 tgcagggtgt tcttatgaac ctggtgacca ctggagggtta gataagcgctc  
 16851 tacaagagga ggttatctat gccatgagct tggcattcag ggtcaagcat  
 16901 cgggtcatcag acagttttgc ttgaagatgg cattgccctt gtagcaatgc  
 16951 aggtctctaga gagcttcctg ccctcttgga gctgatgttc cttccagcaa  
 17001 aggaaacagc aagcaattaa aataacaaat aagtacatta cagaagatgg  
 17051 gcaaaagaac aatgaaaagc ccctcagggg ggggacaggg gaggggaggg  
 17101 gggcgccag gcagggcgcg cagtttctaa ataggtggtt ggggtggcgag  
 17151 tattgacagg ctgacgtgtg agcagggaca gggagggagg gagaggtctc  
 17201 gccacagga catctggcaa agagcggtca ggcagagggc acttgaccct  
 17251 gaatgccaag ctcatggcat agatagccga ggcaggcatg caggcactca  
 17301 gagaagggac acgcccggct tgcactttgg aaagctgccc ctactgggaa  
 17351 tgactggcgg gcaggagtcg aagtggaaaa ggagagcaga ggacactgca  
 17401 gccatccagg cgaggggtga tggggctcag cccttgtggt caccttggag  
 17451 gtggggaaca gaggccagat tccaggctct atacctctgc gcctttgtac  
 17501 acgctgttcc ccttacttgg ttgcccttcc ttctgtgtc ggtgttcaga  
 17551 tgcccacttc tcttcatga tctctcccag cctgatgctc tgagcccctg  
 17601 ccatttgcca cagcccttta gagcgctgg cacagggtt cctagcagat  
 17651 tggtgacatt tctggctcca ctgcccata tcaggcccaa gatcggtgg  
 17701 gcaggttcca cgtcctctct gtcttgggt tgcagcgccc agcaggaggc  
 17751 agcaatggag aactgggtgc aggagggaca ggcccaccca ggctcatgcc  
 17801 tggacttggc cttggctgcc ctccagctcc cctaccgac acccgtcacc  
 17851 ccggtctaga ttccattcca gagaatgagc attcagctgt tctcccaacc  
 17901 caccctccag cccgcctcgc tgcttcccc caggggaagg aaccacagg  
 17951 gaatgggat ctccgctcac acttaccatg ggggatacag ggtgttagg  
 18001 atcttgcaac tgagctccta acaccaccc cactgccac cccacctcc  
 18051 cagGTCCCTG AAGAAGTCTG GTGACATCTG GCTGGACGCC TACCTCCATC  
 18101 AGTGAAGGCA ACACCCAGGC GGCAGAGAA GGGCTCAGGG CACCAGCAAC  
 18151 CAAGCCAGCC CCGGGCGGGA TCGATACCC CACCCCTCCA CTGGCCAGCC  
 18201 TGGGGGTGCC CTGCCGTGCC TCCTGGTACT GTTGCTTCC CCTCGGCCCC  
 18251 CTCACATGTG TATTCAGCAG CCCTATGGCC TTGGCTCTGG GCCTGATGGG  
 18301 ACAGGGGTAG AGGGAAGGTG AGCATAGCAC ATTTTCCTAG AGCGAGAATT  
 18351 GGGGGAAAGC TGTTATTTTT ATATTAAAT ACATTCAGAT GTATTATGGA  
 18401 GT

FIG.2G

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|     |   |     |
|-----|---|-----|
| 1   | CTTCGCTTCCCTCGGGGTCTTGCTCGGACCTCGGCCACCGCCTGGGATCC  | 50  |
| 51  | CCAGGACTCGTGCCTGCAGCATGGGCGGCGTCGGGGAGCCGGGACCGCGG  | 100 |
| 1   | M G G V G E P G P R                                 | 10  |
| 101 | GAGGGACCCGCGCAGCCGGGGGACCGCTGCCACCTTCTGCTGGGAGCA    | 150 |
| 11  | E G P A Q P G A P L P T F C W E Q                   | 27  |
| 151 | GATCCGCGCGCACGACCAGCCCGGCGACAAGTGGCTGGTCATCGAGCGCC  | 200 |
| 28  | I R A H D Q P G D K W L V I E R R                   | 44  |
| 201 | GCGTCTACGACATCAGCCGCTGGGCACAGCGGCACCCAGGGGGCAGCCGC  | 250 |
| 45  | V Y D I S R W A Q R H P G G S R                     | 60  |
| 251 | CTCATCGGCCACCACGGCGCTGAGGACGCCACGGATGCCTTCCGTGCCTT  | 300 |
| 61  | L I G H H G A E D A T D A F R A F                   | 77  |
| 301 | CCATCAAGATCTCAATTTTGTGCGCAAGTTCCTACAGCCCCTGTTGATTG  | 350 |
| 78  | H Q D L N F V R K F L Q P L L I G                   | 94  |
| 351 | GAGAGCTGGCTCCGGAAGAAGCCAGCCAGGATGGACCCCTGAATGCGCAG  | 400 |
| 95  | E L A P E E P S Q D G P L N A Q                     | 110 |
| 401 | CTGGTCGAGGACTTCCGAGCCCTGCACCAGGCAGCCGAGGACATGAAGCT  | 450 |
| 111 | L V E D F R A L H Q A A E D M K L                   | 127 |
| 451 | GTTTGATGCCAGTCCCACCTTCTTTGCTTTCCTACTGGGCCACATCCTGG  | 500 |
| 128 | F D A S P T F F A F L L G H I L A                   | 144 |
| 501 | CCATGGAGGTGCTGGCCTGGCTCCTTATCTACCTCCTGGGTCTGGCTGG   | 550 |
| 145 | M E V L A W L L I Y L L G P G W                     | 160 |
| 551 | GTGCCCAGTGCCCTGGCCGCCTTCATCCTGGCCATCTCTCAGGCTCAGTC  | 600 |
| 161 | V P S A L A A F I L A I S Q A Q S                   | 177 |
| 601 | CTGGTGTCTGCAGCATGACCTGGGCCATGCCTCCATCTTCAAGAAGTCCT  | 650 |
| 178 | W C L Q H D L G H A S I F K K S W                   | 194 |
| 651 | GGTGGAACCACGTGGCCCCAGAAGTTCGTGATGGGGCAGCTAAAGGGCTTC | 700 |
| 195 | W N H V A Q K F V M G Q L K G F                     | 210 |

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FIG.3A

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|      |   |      |
|------|---|------|
| 701  | TCGCCCCACTGGTGGAACTTCCGCCACTTCCAGCACCACGCCAAGCCCA   | 750  |
| 211  | S A H W W N F R H F Q H H A K P N                   | 227  |
| 751  | CATCTTCCACAAAGACCCAGACGTGACGGTGGCGCCCGTCTTCCTCCTGG  | 800  |
| 228  | I F H K D P D V T V A P V F L L G                   | 244  |
| 801  | GGGAGTCATCCGTCGAGTATGGCAAGAAGAAACGCAGATACCTACCCTAC  | 850  |
| 245  | E S S V E Y G K K K R R Y L P Y                     | 260  |
| 851  | AACCAGCAGCACCTGTACTTCTTCTGATCGGCCCGCCGCTGCTCACCTT   | 900  |
| 261  | N Q Q H L Y F F L I G P P L L T L                   | 277  |
| 901  | GGTGAAC TTTGAAGTGGAAAATCTGGCGTACATGCTGGTGTGCATGCAGT | 950  |
| 278  | V N F E V E N L A Y M L V C M Q W                   | 294  |
| 951  | GGGCGGATTTGCTCTGGGCCGCCAGCTTCTATGCCCCGCTTCTTCTTATCC | 1000 |
| 295  | A D L L W A A S F Y A R F F L S                     | 310  |
| 1001 | TACCTCCCCTTCTACGGCGTCCCTGGGGTGCTGCTCTTCTTTGTTGCTGT  | 1050 |
| 311  | Y L P F Y G V P G V L L F F V A V                   | 327  |
| 1051 | CAGGGTCCTGGAAGCCACTGGTTCGTGTGGATCACACAGATGAACCACA   | 1100 |
| 328  | R V L E S H W F V W I T Q M N H I                   | 344  |
| 1101 | TCCCCAAGGAGATCGGCCACGAGAAGCACCGGGACTGGGTACAGCTCTCAG | 1150 |
| 345  | P K E I G H E K H R D W V S S Q                     | 360  |
| 1151 | CTGGCAGCCACCTGCAACGTGGAGCCCTCACTTTTCACCAACTGGTTCAG  | 1200 |
| 361  | L A A T C N V E P S L F T N W F S                   | 377  |
| 1201 | CGGGCACCTCAACTTCCAGATCGAGCACCACCTCTTCCCCAGGATGCCGA  | 1250 |
| 378  | G H L N F Q I E H H L F P R M P R                   | 394  |
| 1251 | GACACAAC TACAGCCGGGTGGCCCCGCTGGTCAAGTCGCTGTGTGCCAAG | 1300 |
| 395  | H N Y S R V A P L V K S L C A K                     | 410  |
| 1301 | CACGGCCTCAGCTACGAAGTGAAGCCCTTCTCACC GCGCTGGTGGACAT  | 1350 |
| 411  | H G L S Y E V K P F L T A L V D I                   | 427  |
| 1351 | CGTCAGGTCCCTGAAGAAGTCTGGTGACATCTGGCTGGACGCCTACCTCC  | 1400 |
| 428  | V R S L K K S G D I W L D A Y L H                   | 444  |

FIG.3B



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|      |  |      |
|------|--|------|
| 1401 | ATCAGTGAAGGCAACACCCAGGCGGGCAGAGAAGGGCTCAGGGCACCAGC | 1450 |
| 445  | Q  | 445  |
| 1451 | AACCAAGCCAGCCCCCGGCGGGATCGATACCCCCACCCTCCACTGGCCA  | 1500 |
| 1501 | GCCTGGGGGTGCACTGCCTGCCCTCCTGGTACTGTTGTCTTCCCCTCGGC | 1550 |
| 1551 | CCCCTCACATGTGTATTCAGCAGCCCTATGGCCTTGGCTCTGGGCCTGAT | 1600 |
| 1601 | GGGACAGGGGTAGAGGGAAGGTGAGCATAGCACATTTTCCTAGAGCGAGA | 1650 |
| 1651 | ATTGGGGGAAAGCTGTTATTTTTATATTAATAACATTCAGATGTAAAAA  | 1700 |

FIG.3C

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FIG. 4

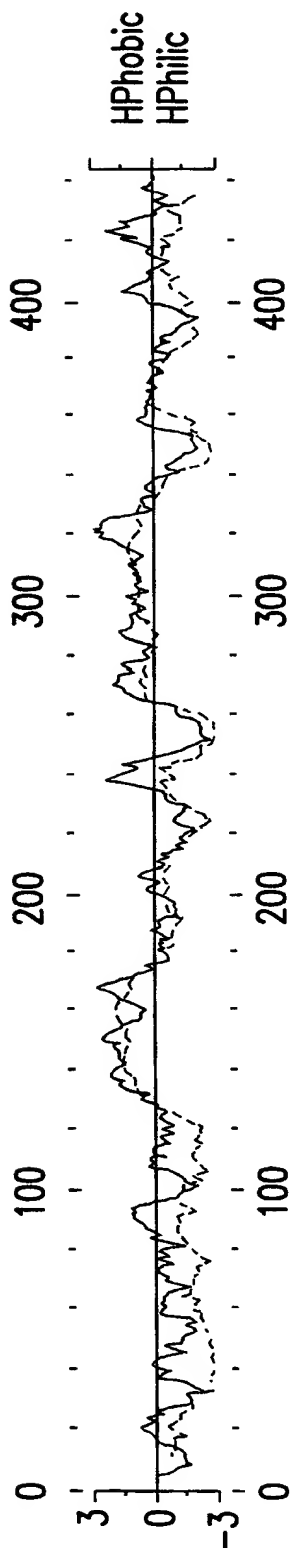


FIG. 5A

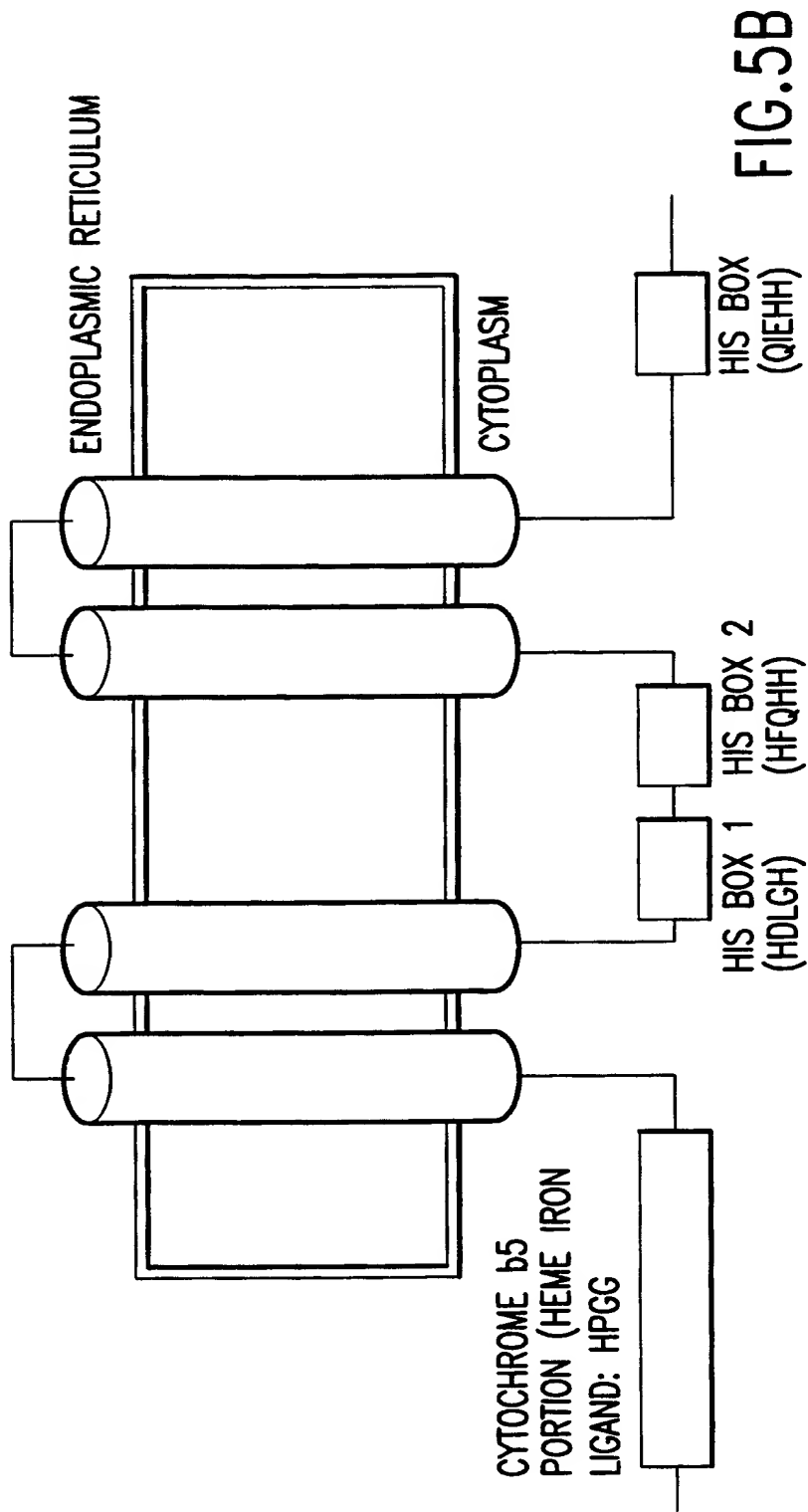


FIG. 5B

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PROFILESCAN of : CYB5rp\_correct\_protein check: 5714 from: 1 to: 445

GETSEQ from bmd, December 2, 1997 14:20.

Compare to profile library: GenRunData:profilesca.n.fil

---

Profile: profiledir:cytochrome\_b5.prfl

Gap weight: 4.50 Gap Length weight: 0.05

Ave match: 0.27 Ave mismatch : -0.21

(Peptide) PROFILEMAKE v4.40 of: 0191.Msf2{\*} Length: 48

Sequences: 24 MaxScore: 27.58 December 2, 1992 00:07

This profile is derived from PROSITE release 10.0 and has been tested by a database search against SWISS-PROT release 26.0. A comparison of the SWISS-PROT annotation and the results of the database search follows. For further information about this motif, consult the . . .

Profile: profiledir:cytochrome\_b5.prfl alignment: 1

Quality: 20.77 Gaps: 0

Ratio: 0.43 Length: 48

Normalized quality: 2.91

```

S   31 HDQPGDKWLVIERRVYDISRWAQRHPGGSRLIGHGAEDATDAFRAFH 78
      |: .: |||. .|||::| . |||. | .|||.|||. :|
P   1 HNDGEETWLVNGQVYDITKFLLEHPGGPDVIMEAAGTDATEEFEAIH 48

```

```

*****
*Cytochrome b5 family, heme-binding domain signature *
*****

```

FIG.6

↑ pir:s68358 hypothetical protein - common sunflower  
Length = 458

Identities = 31/85 (36%), Positives = 49/85 (57%)

His box 3

Sbjct: 348 VGPPKGDNWF EKQTRGTIDACSSWMDWFFGGLQFQLEHLLFPRLPRCHLRSISPICREL 407

C K+ L Y F A V +++L+

Sbjct: 408 CKKYNLPYVSLSFYDANVTTLKTLR 432

Identities = 21/53 (39%), Positives = 35/53 (66%)

HPGG motif

Sbjct: 22 KELKKHNNPNDLWISILGKVVNTEWAKEHPGGDAPLINLAGQDVTDAFIAFH 74

Identities = 25/76 (32%), Positives = 34/76 (44%)

His box 1

His box 2

Sbjct: 152 LSGAILGLAWMQIAYLGHDAGHYQMMATRGWNKFAGIFIGNCITGISIAWKKWTHNAHI 211

N      DPD+      P+

Sb jct: 212 ACNSLDYDPDLQHLPM 227

Identities = 7/14 (50%), Positives = 9/14 (64%)

FIG. 7A

FIG. 7B



FIG. 8

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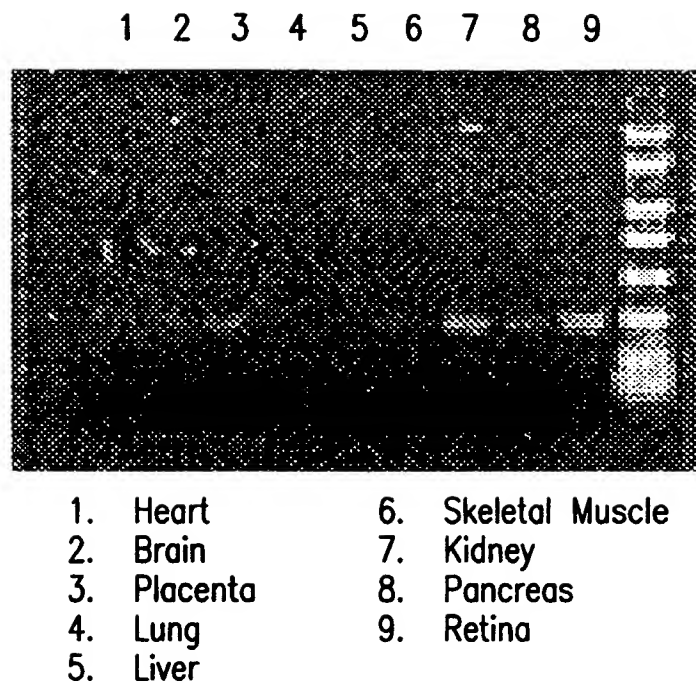
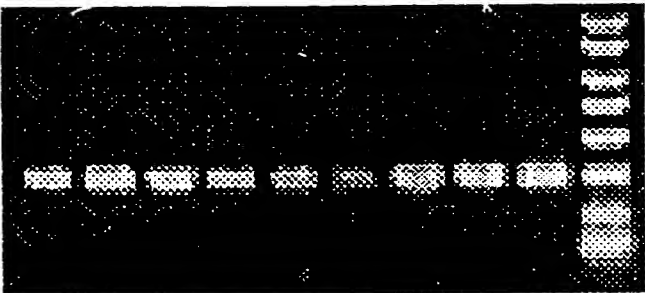


FIG.9A

| Station | Time | Lat       | Long       | Alt | Temp | Hum | Wind | Dir | Speed | Pressure | Clouds | Remarks |
|---------|------|-----------|------------|-----|------|-----|------|-----|-------|----------|--------|---------|
| 1       | 0000 | 34° 00' N | 119° 00' W | 10  | 10.0 | 80  | 10   | 000 | 0.0   | 1013.2   | 000    | Clear   |
| 2       | 0100 | 34° 00' N | 119° 00' W | 10  | 9.5  | 75  | 10   | 000 | 0.0   | 1013.1   | 000    | Clear   |
| 3       | 0200 | 34° 00' N | 119° 00' W | 10  | 9.0  | 70  | 10   | 000 | 0.0   | 1013.0   | 000    | Clear   |
| 4       | 0300 | 34° 00' N | 119° 00' W | 10  | 8.5  | 65  | 10   | 000 | 0.0   | 1012.9   | 000    | Clear   |
| 5       | 0400 | 34° 00' N | 119° 00' W | 10  | 8.0  | 60  | 10   | 000 | 0.0   | 1012.8   | 000    | Clear   |
| 6       | 0500 | 34° 00' N | 119° 00' W | 10  | 7.5  | 55  | 10   | 000 | 0.0   | 1012.7   | 000    | Clear   |
| 7       | 0600 | 34° 00' N | 119° 00' W | 10  | 7.0  | 50  | 10   | 000 | 0.0   | 1012.6   | 000    | Clear   |
| 8       | 0700 | 34° 00' N | 119° 00' W | 10  | 6.5  | 45  | 10   | 000 | 0.0   | 1012.5   | 000    | Clear   |
| 9       | 0800 | 34° 00' N | 119° 00' W | 10  | 6.0  | 40  | 10   | 000 | 0.0   | 1012.4   | 000    | Clear   |
| 10      | 0900 | 34° 00' N | 119° 00' W | 10  | 5.5  | 35  | 10   | 000 | 0.0   | 1012.3   | 000    | Clear   |
| 11      | 1000 | 34° 00' N | 119° 00' W | 10  | 5.0  | 30  | 10   | 000 | 0.0   | 1012.2   | 000    | Clear   |
| 12      | 1100 | 34° 00' N | 119° 00' W | 10  | 4.5  | 25  | 10   | 000 | 0.0   | 1012.1   | 000    | Clear   |
| 13      | 1200 | 34° 00' N | 119° 00' W | 10  | 4.0  | 20  | 10   | 000 | 0.0   | 1012.0   | 000    | Clear   |
| 14      | 1300 | 34° 00' N | 119° 00' W | 10  | 3.5  | 15  | 10   | 000 | 0.0   | 1011.9   | 000    | Clear   |
| 15      | 1400 | 34° 00' N | 119° 00' W | 10  | 3.0  | 10  | 10   | 000 | 0.0   | 1011.8   | 000    | Clear   |
| 16      | 1500 | 34° 00' N | 119° 00' W | 10  | 2.5  | 5   | 10   | 000 | 0.0   | 1011.7   | 000    | Clear   |
| 17      | 1600 | 34° 00' N | 119° 00' W | 10  | 2.0  | 0   | 10   | 000 | 0.0   | 1011.6   | 000    | Clear   |
| 18      | 1700 | 34° 00' N | 119° 00' W | 10  | 1.5  | 0   | 10   | 000 | 0.0   | 1011.5   | 000    | Clear   |
| 19      | 1800 | 34° 00' N | 119° 00' W | 10  | 1.0  | 0   | 10   | 000 | 0.0   | 1011.4   | 000    | Clear   |
| 20      | 1900 | 34° 00' N | 119° 00' W | 10  | 0.5  | 0   | 10   | 000 | 0.0   | 1011.3   | 000    | Clear   |
| 21      | 2000 | 34° 00' N | 119° 00' W | 10  | 0.0  | 0   | 10   | 000 | 0.0   | 1011.2   | 000    | Clear   |
| 22      | 2100 | 34° 00' N | 119° 00' W | 10  | -0.5 | 0   | 10   | 000 | 0.0   | 1011.1   | 000    | Clear   |
| 23      | 2200 | 34° 00' N | 119° 00' W | 10  | -1.0 | 0   | 10   | 000 | 0.0   | 1011.0   | 000    | Clear   |
| 24      | 2300 | 34° 00' N | 119° 00' W | 10  | -1.5 | 0   | 10   | 000 | 0.0   | 1010.9   | 000    | Clear   |
| 25      | 0000 | 34° 00' N | 119° 00' W | 10  | -2.0 | 0   | 10   | 000 | 0.0   | 1010.8   | 000    | Clear   |



**FIG. 9B**